

## POPULATION GENETIC ANALYSIS OF MOUNTAIN PLOVER USING MITOCHONDRIAL DNA SEQUENCE DATA

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**Abstract.** Mountain Plover (*Charadrius montanus*) distribution and abundance have been reduced drastically in the past 30 years and the conversion of shortgrass prairie to agriculture has caused breeding populations to become geographically isolated. This, coupled with the fact that Mountain Plovers are thought to show fidelity to breeding grounds, leads to the prediction that the isolated breeding populations would be genetically distinct. This pattern, if observed, would have important management implications for a species at risk of extinction. Our study examined genetic variation at two mitochondrial regions for 20–30 individuals from each of four breeding sites. We found no evidence of significant population differentiation in the data from the control region or the ATPase 6/8 region. Nested-clade analysis revealed no relationship between haplotype, phylogeny, and geography among the 47 control region haplotypes. In the ATPase 6/8 region, however, one of the two clades provided information suggesting that, historically, there has been continuous range expansion. Analysis of mismatch distributions and Tajima's D suggest that the Mountain Plover underwent a population expansion, following the Pleistocene glacial period. To explain the lack of detectable genetic differentiation among populations, despite their geographic isolation and fidelity to breeding locations, we speculate that there is sufficient female-mediated gene flow to homogenize gene pools among populations. Such gene flow might ensue if pair bonds are formed in mixed flocks on wintering grounds rather than on the summer breeding grounds.

**Key words:** *Charadrius montanus*, *gene flow*, *genetic diversity*, *mitochondrial DNA*, *Mountain Plover*, *population genetics*.